

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/756,18604 CO
OIPE 03/13/01
DATE: 03/22/2001
TIME: 23:09:14
#0100

INPUT SET: S36550.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2

3 (1) General Information:

4
5 (i) APPLICANT: Campbell, Robert K.
6 Jameson, Bradford A.
7 Chappel, Scott C.8
9 (ii) TITLE OF INVENTION: HYBRID PROTEINS10
11 (iii) NUMBER OF SEQUENCES: 2212
13 (iv) CORRESPONDENCE ADDRESS:14
15 (A) ADDRESSEE: BROWDY AND NEIMARK
16 (B) STREET: 419 Seventh Street N.W., Ste. 300
17 (C) CITY: Washington
18 (D) STATE: D.C.
19 (E) COUNTRY: USA
20 (F) ZIP: 2220721
22 (v) COMPUTER READABLE FORM:23
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.3028
29 (vi) CURRENT APPLICATION DATA:30
31 (A) APPLICATION NUMBER: 09/756,186
(B) FILING DATE:
(C) CLASSIFICATION:32
33 (vii) PRIOR APPLICATION DATA:34
35 (A) APPLICATION NUMBER: 08/804,166
(B) FILING DATE:
(C) CLASSIFICATION:36
37 (viii) ATTORNEY/AGENT INFORMATION:38
39 (A) NAME: Browdy, Roger L.
40 (B) REGISTRATION NUMBER: 25,618
41 (C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A42
43 (ix) TELECOMMUNICATION INFORMATION:44
45 (A) TELEPHONE: (202) 628-5197
(B) TELEFAX: (202) 737-3528

46 (2) INFORMATION FOR SEQ ID NO:1:

ENTERED

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/756,186**

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47     (i) SEQUENCE CHARACTERISTICS:
48         (A) LENGTH: 1049 base pairs
49         (B) TYPE: nucleic acid
50         (C) STRANDEDNESS: single
51         (D) TOPOLOGY: linear
52
53     (ii) MOLECULE TYPE: cDNA
54
55     (ix) FEATURE:
56         (A) NAME/KEY: CDS
57         (B) LOCATION: 278..1047
58
59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 TCCACATGGC TACAGGTAAG CGCCCTAAA ATCCCTTGG GCACAATGTG TCCTGAGGGG 60
62
63 AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCCT CAGGTTTGGG GCTTCTCAAT 120
64
65 CTCACTATCG CCATGTAAGC CCAGTATTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA 180
66
67 GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGGA GAGTGCTGGC CTCTTGCTCT 240
68
69 CCGGCTCCCT CTGTTGCCCT CTGGTTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC 295
70                     Ser Arg Thr Ser Leu Leu
71                     1           5
72
73 CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC 343
74 Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
75           10          15          20
76
77 GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCC 391
78 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
79           25          30          35
80
81 ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT 439
82 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
83           40          45          50
84
85 CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC 487
86 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
87           55          60          65          70
88
89 TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA 535
90 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
91           75          80          85
92
93 TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC 583
94 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
95           90          95          100
96
97 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG 631
98 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
99           105         110         115

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100	AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG	679
101	Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly	
102	120 125 130	
104		
105	ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC	727
106	Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys	
107	135 140 145 150	
108		
109	CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCC GGT	775
110	His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala Gly	
111	155 160 165	
112		
113	GCT GCC CCA GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC	823
114	Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe	
115	170 175 180	
116		
117	TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT	871
118	Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser	
119	185 190 195	
120		
121	AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA	919
122	Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln	
123	200 205 210	
124		
125	AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC	967
126	Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn	
127	215 220 225 230	
128		
129	AGG GTC ACA GTC ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GGG TGC	1015
130	Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Gly Cys	
131	235 240 245	
132		
133	CAC TGC AGT ACT TGT TAT TAT CAC AAA TCT TA AG	1049
134	His Cys Ser Thr Cys Tyr Tyr His Lys Ser	
135	250 255	
136		
137		
138		
139		
140	(2) INFORMATION FOR SEQ ID NO:2:	
141		
142	(i) SEQUENCE CHARACTERISTICS:	
143	(A) LENGTH: 256 amino acids	
144	(B) TYPE: amino acid	
145	(D) TOPOLOGY: linear	
146		
147	(ii) MOLECULE TYPE: protein	
148		
149	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
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151	Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp	
152	1 5 10 15	

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153
154 Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
155 20 25 30
156
157 His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
158 35 40 45
159
160 Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
161 50 55 60
162
163 Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
164 65 70 75 80
165
166 Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
167 85 90 95
168
169 Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
170 100 105 110
171
172 Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
173 115 120 125
174
175 Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
176 130 135 140
177
178 Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
179 145 150 155 160
180
181 Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu
182 165 170 175
183
184 Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys
185 180 185 190
186
187 Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys
188 195 200 205
189
190 Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys
191 210 215 220
192
193 Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val
194 225 230 235 240
195
196 Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
197 245 250 255
198
199
200 (2) INFORMATION FOR SEQ ID NO:3:
201
202 (i) SEQUENCE CHARACTERISTICS:
203 (A) LENGTH: 1202 base pairs
204 (B) TYPE: nucleic acid
205 (C) STRANDEDNESS: single

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206 (D) TOPOLOGY: linear
 207
 208 (ii) MOLECULE TYPE: cDNA
 209
 210 (ix) FEATURE:
 211 (A) NAME/KEY: CDS
 212 (B) LOCATION: 279..1199
 213
 214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 215
 216 CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTG GGCACAATGT GTCCTGAGGG 60
 217
 218 GAGAGGTAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TGAGGTTTGG GGCTTCTGAA 120
 219
 220 TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG 180
 221
 222 AGGGATGGAG AGAGAAAAAC AAACAGCTCC TGGAGCAGGG AGAGTGCTGG CCTCTTGCTC 240
 223
 224 TCCGGCTCCC TCTGTTGCC C TGTGGTTCT CCCCAGGC TCC CGG ACG TCC CTG 293
 225 Ser Arg Thr Ser Leu
 226 260
 227
 228 CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT 341
 229 Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser
 230 265 270 275
 231
 232 GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT 389
 233 Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
 234 280 285 290
 235
 236 TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC 437
 237 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
 238 295 300 305
 239
 240 TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC 485
 241 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
 242 310 315 320 325
 243
 244 TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC 533
 245 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
 246 330 335 340
 247
 248 AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG 581
 249 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
 250 345 350 355
 251
 252 GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT 629
 253 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
 254 360 365 370
 255
 256 TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT 677
 257 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
 258 375 380 385

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SEQUENCE VERIFICATION REPORT
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Line

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Original Text